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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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09/292,437 04/15/99 SCHNEEWIND

0 510015.213

HM22/1004

MICHAEL B FARBER
OPPENHEIMER WOLFF & DONNELLY
2029 CENTURY PARK EAST 38TH FLOOR
LOS ANGELES CA 90067-3024

EXAMINER

NAVARRO, A

ART UNIT

PAPER NUMBER

1645

DATE MAILED:

10/04/00

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
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Washington, D.C. 20231

DEA/PCE-1994

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER
	12

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

The reply filed July 24, 2000 is not fully responsive to the communication mailed June 19, 2000 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report.

Since the above-mentioned reply appears to be *bona fide*, applicant is given a TIME PERIOD of ONE (1) MONTH or THIRTY (30) DAYS, from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME LIMIT MAY BE GRANTED UNDER 37 CFR 1.136(a).


Mark Navarro

Primary Examiner

September 12, 2000

Application No.: 09/292,437

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s)

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/292,437

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 J Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 J Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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A. Navarro

Page 1 of 3

RAW SEQUENCE LISTING DATE: 07/31/2000
PATENT APPLICATION: US/09/292,437 TIME: 15:11:23

Input Set : A:\510015-213 Rev Seq Listing.txt
Output Set: N:\CRF3\07312000\I292437.raw

4 <110> APPLICANT: Olaf Schneewind
5 Sarkis Mazmanian
6 Gwen Liu
7 Hung Ton-That
9 <120> TITLE OF INVENTION: TITLE OF INVENTION: IDENTIFICATION OF SORTASE GENE
12 <130> FILE REFERENCE: FILE REFERENCE: 510015-213
W--> 13 <140> CURRENT APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/292,437
C--> 14 <141> CURRENT FILING DATE: 1999-04-15
E--> 15 <160> NUMBER OF SEQ ID: NUMBER OF SEQ ID NOS: 36
E--> 15 <160> NUMBER OF SEQ ID NOS: NUMBER OF SEQ ID NOS: 36
17 <170> SOFTWARE: SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

E--> 19 <210> SEQ ID NO: SEQ ID NO 1
20 <211> LENGTH: LENGTH: 5
E--> 21 <212> TYPE: TYPE: PRT
22 <213> ORGANISM: ORGANISM: Bacteria
E--> 24 <400> SEQUENCE: SEQUENCE: 1
25 Leu Pro Xaa Thr Gly
26 1 1 5 1

misaligned amino acid numbers.

see item 10 on Env Summary sheet

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Does Not Comply
Corrected Diskette Needed

all
numeric identifiers
from <120> through
Sequence 36
have alphabetical
headings, too. Please
show ONLY the
numeric identifiers.
The new sequence
headers require
only the numeric
identifiers. The
CRF program
inserts the
alphabetical headings
as it is processing
the file.

VERIFICATION SUMMARY

DATE: 07/31/2000

PATENT APPLICATION: US/09/292,437

TIME: 15:11:25

Input Set : A:\510015-213 Rev Seq Listing.txt

Output Set: N:\CRF3\07312000\I292437.raw

L:13 M:283 W: Missing Blank Line separator, <140> field identifier
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:283 W: Missing Blank Line separator, <160> field identifier
L:15 M:212 E: (34) Invalid or duplicate Sequence ID Number, Number Of Sequences Unknown
L:19 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:21 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:24 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:34 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:445 M:283 W: Missing Blank Line separator, <400> field identifier
L:15 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (36)